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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	648	39.9	317	1	US-08-748-068-3	Sequence 3, Appli
2	635	39.1	322	4	US-09-710-279-1412	Sequence 1412, Ap
3	635	39.1	322	4	US-09-710-279-2384	Sequence 2384, Ap
4	635	39.1	330	3	US-09-134-001C-4328	Sequence 4328, Ap
5	599	36.9	324	4	US-09-107-532A-6486	Sequence 6486, Ap
6	585	36.0	318	4	US-09-134-000C-4417	Sequence 4417, Ap
7	578	35.6	331	4	US-09-711-681-4	Sequence 4, Appli
8	578	35.6	331	4	US-10-274-266-4	Sequence 4, Appli
9	576.5	35.5	332	4	US-09-583-110-4591	Sequence 4591, Ap

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 18, 2005, 18:27:31 ; Search time 40 Seconds
(without alignments)
535.518 Million cell updates/sec

Title: US-09-992-430B-22
Perfect score: 323
Sequence: 1 MFQDTKSQAVRTDAKTVKVV.....ELMEKSASQIKSVIEHLEIN 323

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	3.1	322	4	US-09-710-279-1412	Sequence 1412, Ap
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3	10	3.1	330	3	US-09-134-001C-4328	Sequence 4328, Ap
4	8	2.5	318	4	US-09-134-000C-4417	Sequence 4417, Ap
5	8	2.5	332	4	US-09-583-110-4591	Sequence 4591, Ap
6	8	2.5	381	4	US-09-602-787A-178	Sequence 178, App
7	7	2.2	20	1	US-08-218-025A-76	Sequence 76, Appl
8	7	2.2	63	4	US-09-513-999C-6104	Sequence 6104, Ap
9	7	2.2	83	4	US-09-583-110-3448	Sequence 3448, Ap
10	7	2.2	93	3	US-08-965-056-56	Sequence 56, Appl
11	7	2.2	94	3	US-08-965-056-57	Sequence 57, Appl

12	7	2.2	138	4	US-09-570-921-9	Sequence 9, Appli
13	7	2.2	138	4	US-09-570-921-11	Sequence 11, Appl
14	7	2.2	138	4	US-09-570-921-12	Sequence 12, Appl
15	7	2.2	138	4	US-09-570-921-15	Sequence 15, Appl
16	7	2.2	149	3	US-09-433-428D-67	Sequence 67, Appl
17	7	2.2	159	4	US-09-248-796A-20273	Sequence 20273, A
18	7	2.2	160	3	US-09-433-428D-70	Sequence 70, Appl
19	7	2.2	169	4	US-09-248-796A-19124	Sequence 19124, A
20	7	2.2	181	1	US-08-307-499-58	Sequence 58, Appl
21	7	2.2	181	3	US-09-299-268-58	Sequence 58, Appl
22	7	2.2	220	3	US-09-433-428D-66	Sequence 66, Appl
23	7	2.2	233	3	US-08-965-056-49	Sequence 49, Appl
24	7	2.2	233	3	US-08-965-056-50	Sequence 50, Appl
25	7	2.2	267	3	US-08-965-056-11	Sequence 11, Appl
26	7	2.2	267	3	US-08-965-056-15	Sequence 15, Appl
27	7	2.2	268	3	US-08-965-056-8	Sequence 8, Appli
28	7	2.2	268	3	US-08-965-056-10	Sequence 10, Appl
29	7	2.2	268	3	US-08-965-056-13	Sequence 13, Appl
30	7	2.2	268	3	US-08-965-056-39	Sequence 39, Appl
31	7	2.2	268	3	US-08-965-056-41	Sequence 41, Appl
32	7	2.2	269	3	US-08-965-056-12	Sequence 12, Appl
33	7	2.2	269	3	US-08-965-056-22	Sequence 22, Appl
34	7	2.2	269	3	US-08-965-056-23	Sequence 23, Appl
35	7	2.2	269	3	US-08-965-056-42	Sequence 42, Appl
36	7	2.2	269	3	US-08-965-056-46	Sequence 46, Appl
37	7	2.2	304	4	US-09-634-238-238	Sequence 238, App
38	7	2.2	307	4	US-09-107-532A-4274	Sequence 4274, Ap
39	7	2.2	317	1	US-08-748-068-3	Sequence 3, Appli
40	7	2.2	317	2	US-08-864-799-4	Sequence 4, Appli
41	7	2.2	317	2	US-08-864-799-5	Sequence 5, Appli
42	7	2.2	317	4	US-09-252-991A-22489	Sequence 22489, A
43	7	2.2	324	4	US-09-107-532A-6486	Sequence 6486, Ap
44	7	2.2	327	4	US-09-489-039A-14052	Sequence 14052, A
45	7	2.2	329	1	US-08-270-013B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-710-279-1412
; Sequence 1412, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1412
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence

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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-09-710-279-1412

  Query Match             3.1%;  Score 10;  DB 4;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        150 RVIGSGTVLD 159
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Db        148 RVIGSGTVLD 157


RESULT 2
US-09-710-279-2384
; Sequence 2384, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2384
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-09-710-279-2384

  Query Match             3.1%;  Score 10;  DB 4;  Length 322;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        150 RVIGSGTVLD 159
              ||||||||||
Db        148 RVIGSGTVLD 157


RESULT 3
US-09-134-001C-4328
; Sequence 4328, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
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7: geneseqp2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1614.5	99.4	324	5	AAE25510	Aae25510 Kluyverom
2	952.5	58.6	313	5	AAE25511	Aae25511 Torulaspo
3	723.5	44.5	318	6	ABR82282	Abr82282 B. megate
4	663	40.8	319	5	AAE23265	Aae23265 Bacillus
5	654	40.2	319	2	AAR10591	Aar10591 L-lactic
6	646.5	39.8	317	6	ABM72014	Abm72014 Staphyloc
7	639	39.3	321	8	ADO59775	Ado59775 B. subtil
8	635	39.1	322	4	AAG82159	Aag82159 S. epider

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1: uniprot_sprot:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	843	51.9	324	2	Q7SES6	Q7ses6 neurospora
2	838	51.6	330	1	LDH_SCHPO	Q9p7p7 schizosacch
3	753	46.3	315	1	LDH_CLOTM	Q8kqc4 clostridium
4	746	45.9	316	1	LDH_CLOTE	Q892u0 clostridium
5	733	45.1	313	1	LDH1_CLOAB	Q97md1 clostridium
6	723.5	44.5	318	1	LDH_BACME	P00345 bacillus me
7	722	44.4	317	1	LDH_CLOPE	Q8xp62 clostridium
8	690	42.5	314	1	LDH1_BACAN	Q81rw4 bacillus an
9	690	42.5	314	1	LDH1_BACC1	P62047 bacillus ce
10	690	42.5	314	2	Q6HK31	Q6hk31 bacillus th
11	690	42.5	314	2	AAT31043	Aat31043 bacillus
12	689	42.4	314	1	LDH1_BACCR	Q81ep4 bacillus ce
13	687.5	42.3	319	1	LDH_THEMA	P16115 thermotoga
14	679	41.8	311	1	LDH_THESA	Q7x5c9 thermoanaer
15	679	41.8	318	1	LDHP_BACPS	P14561 bacillus ps
16	673	41.4	319	1	LDHX_BACPS	P20619 bacillus ps
17	667.5	41.1	317	2	Q9S0N0	Q9s0n0 bacillus st
18	667	41.0	314	1	LDH2_BACAN	Q81k80 bacillus an
19	667	41.0	314	2	Q6HC14	Q6hc14 bacillus th
20	667	41.0	314	2	AAT34253	Aat34253 bacillus
21	667	41.0	317	1	LDH_BACCA	P10655 bacillus ca

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3: pir3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	838	51.6	330	2	T50135	probable l-lactate
2	733	45.1	313	2	E96932	L-lactate dehydrog
3	723.5	44.5	318	1	DEBSLM	L-lactate dehydrog
4	687.5	42.3	319	2	S36863	L-lactate dehydrog
5	679	41.8	318	2	S08182	L-lactate dehydrog
6	673	41.4	319	2	S08183	L-lactate dehydrog
7	669	41.2	317	2	S00019	L-lactate dehydrog
8	667.5	41.1	317	2	T44580	lactate dehydrogen
9	659	40.6	317	2	B29704	L-lactate dehydrog
10	649	39.9	310	2	A84142	L-lactate dehydrog
11	648	39.9	317	1	DEBSLF	L-lactate dehydrog
12	647.5	39.8	317	2	D89787	L-lactate dehydrog
13	639.5	39.4	326	1	DELBLA	L-lactate dehydrog
14	639	39.3	321	2	E69649	L-lactate dehydrog
15	627	38.6	314	2	H86671	L-lactate dehydrog
16	617	38.0	313	2	AC1101	L-lactate dehydrog
17	617	38.0	313	2	AC1463	L-lactate dehydrog

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4: gb_om:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	972	100.0	2229	6	AX593601	AX593601 Sequence
	3	349	35.9	939	6	AX593587	AX593587 Sequence
c	4	265.4	27.3	30176	8	SPAC186	AL157811 S.pombe c
	5	216.4	22.3	1423	1	BACLDHAA	M22305 B.megateriu
c	6	205.2	21.1	10029	1	AE006274	AE006274 Lactococc
	7	201.2	20.7	11158	1	AE007540	AE007540 Clostridi
c	8	200.6	20.6	301439	1	AE015943	AE015943 Clostridi

Database : N_Geneseq_23Sep04:*
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7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		972	100.0	972	6	AAD41577	Aad41577 Kluyverom
2		972	100.0	2229	6	AAD41597	Aad41597 Promoter-
3		349	35.9	939	6	AAD41584	Aad41584 Torulaspo
4		216.4	22.3	957	9	ACF35756	Acf35756 B. megate
5	c	205.2	21.1	110000	6	ABA90521_03	Continuation (4 of
6		196.6	20.2	975	10	ADC93205	Adc93205 E. faeciu
7		191.4	19.7	957	10	ADH83127	Adh83127 Enterococ
8		186.2	19.2	28690	2	AAX13075	Aax13075 Enterococ
9		186.2	19.2	28690	6	ABS98870	Abs98870 Enterococ
10		183.8	18.9	969	4	AAH53009	Aah53009 S. epider
11		183.8	18.9	969	4	AAH53495	Aah53495 S. epider

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3: gb_htc:*
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5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	144.4	14.9	1227	3	CR725013	CR725013 Tetraodon
	3	144.4	14.9	1277	3	CR726668	CR726668 Tetraodon
	4	144.4	14.9	1279	3	CR727091	CR727091 Tetraodon
	5	142.8	14.7	1993	3	CR685436	CR685436 Tetraodon
	6	142.2	14.6	967	7	CK271702	CK271702 EST717780
	7	140.6	14.5	871	7	CK247148	CK247148 EST730785
	8	138.4	14.2	936	7	CK403761	CK403761 AUF_IfHdk

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	19	2.0	330	4	US-09-270-767-18321	Sequence 18321, A
3	19	2.0	603	4	US-09-540-236-607	Sequence 607, App
4	19	2.0	1146	4	US-09-711-681-1	Sequence 1, Appli
5	19	2.0	1146	4	US-10-274-266-1	Sequence 1, Appli
6	19	2.0	3144	4	US-09-711-681-3	Sequence 3, Appli
7	19	2.0	3144	4	US-10-274-266-3	Sequence 3, Appli

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	2.3	740	9	CL567542	CL567542 OB__Ba003
	2	22	2.3	868	9	CL568644	CL568644 OB__Ba004
c	3	21	2.2	172	6	CB451959	CB451959 706777 MA
c	4	21	2.2	520	2	AW239816	AW239816 pti1c.pk0
c	5	21	2.2	540	7	CO619078	CO619078 DG9-192o1
c	6	21	2.2	546	7	CO631574	CO631574 DG9-62n19
c	7	21	2.2	554	7	CO625588	CO625588 DG9-265e4
c	8	21	2.2	558	7	CO598189	CO598189 DG8-161b2
c	9	21	2.2	566	7	CO688770	CO688770 DG11-24o5